



Docket No.: DEBE:016US
Serial No.: 09/403,262
Inventor(s): Nikolaus Theres
Title: "PLANTS WITH CONTROLLED SIDE-SHOOT FORMATION
AND/OR CONTROLLED ABSCISSION ZONE FORMATION"

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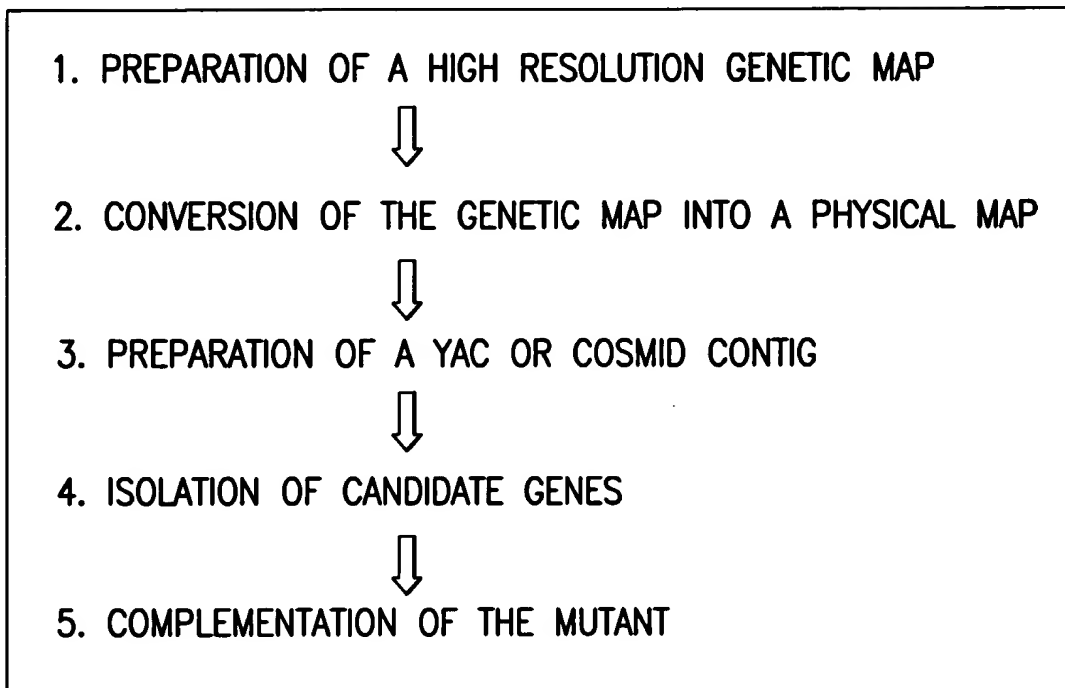


FIG.1



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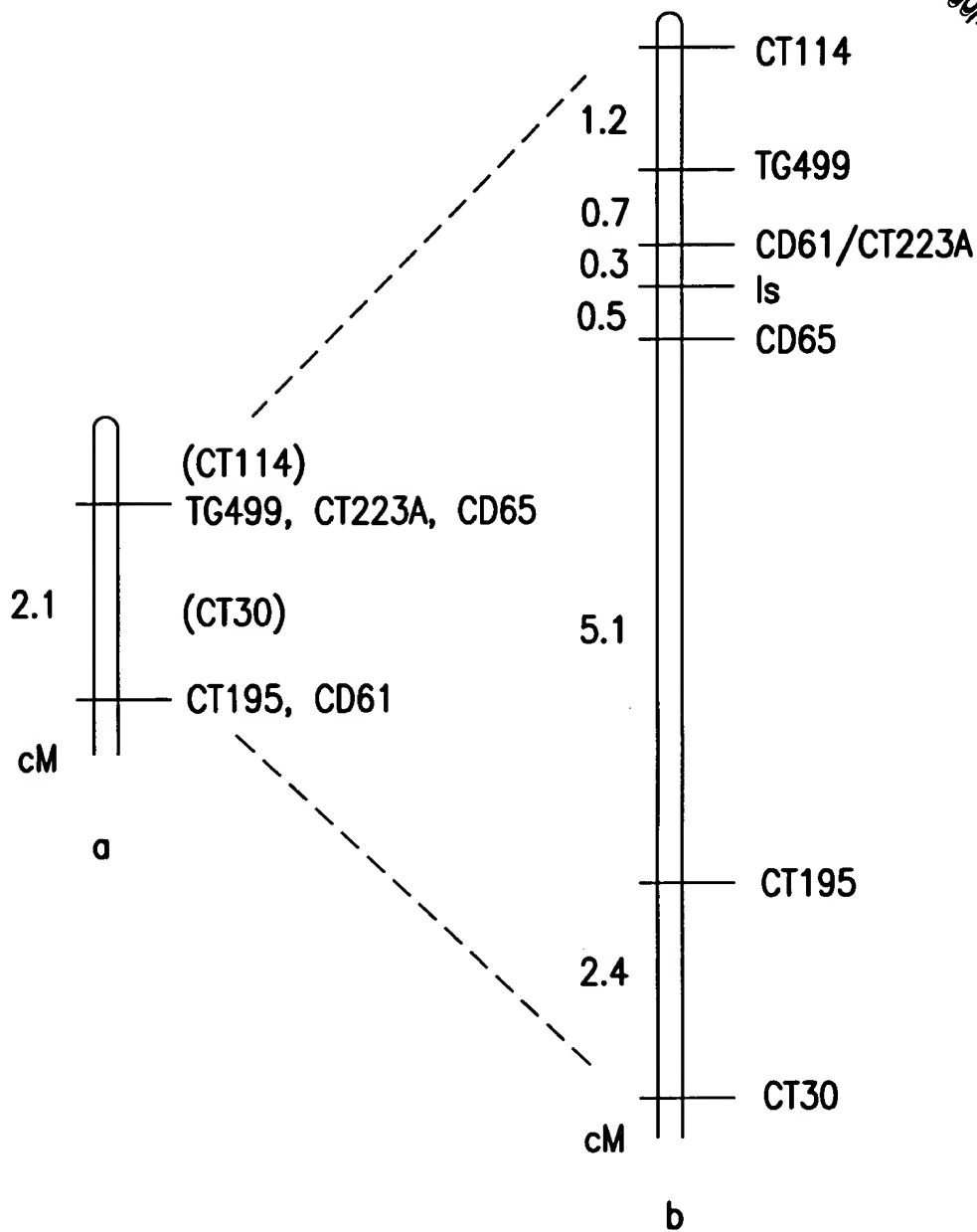


FIG.2



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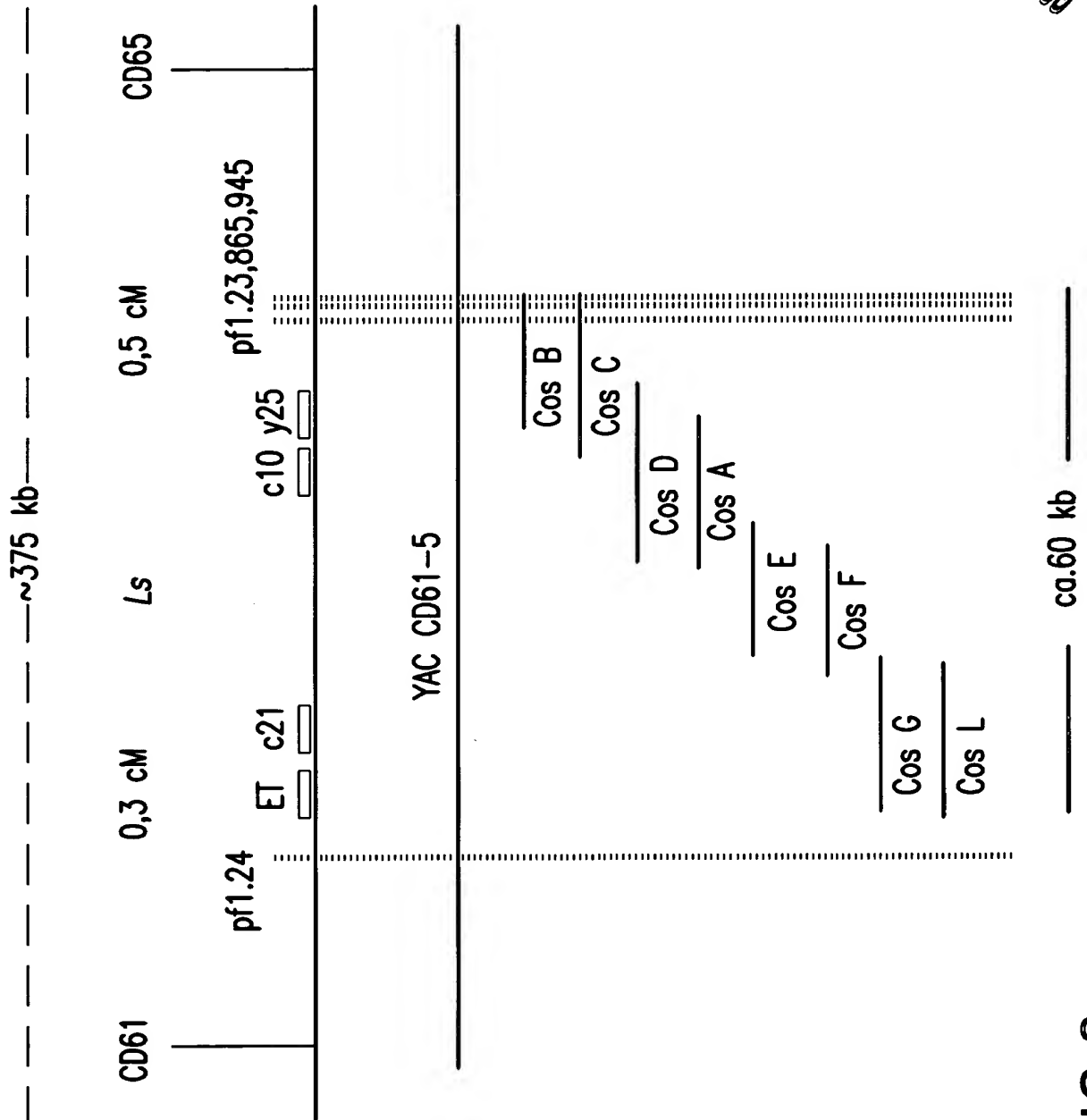
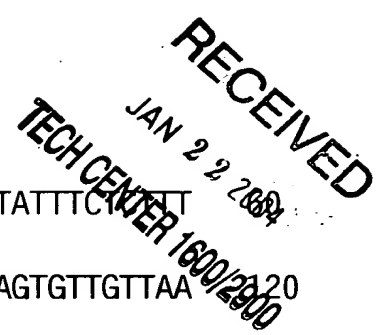


FIG. 3



1 CCTCTGTCCTTCCCCCAGGTCCCCTTTTTTCTTTCTCTCTCCTTTATTTCCTT
61 TCATAAGCATATTCTTTCTCTCTCTAGGGTTTTCACTTTCACCTGAAATAGTGTTGTAA 120
121 ATTGAATGATATGTTAGGATCCTTTGGTTCTTCATCATCTCAATCTCACCTCATCATGA 180
M L G S F G S S S S Q S H P H H D
181 TGAAGAATCTTCTGATCATCATCAACAGCGTAGATTCACCGCTACTGCTACAACATCAC 240
E E S S D H H Q Q R R F T A T A T T I T
241 CACCACCACCATCACTACCTCACCAGCTATTCAAATCCGCCAGCTACTCATTAGCTGTGC 300
T T T I T T S P A I Q I R Q L L I S C A
301 GGAGTTGATTTGCGAGTCCGATTTCTCGGCCGCGAAAAGACTCCTTACTATATTATCAAC 360
E L I S Q S D F S A A K R L L T I L S T
361 TAACTCATCTCCTTTTGGTGATTCAACTGAACGGTTAGTCCATCAATTTACTCGCGCACT 420
N S S P F G D S T E R L V H Q F T R A L
421 TTCCCTTCGTCTCAACCGCTATATATCGTCAACCACCAATCATTTTCATGACACCTGTTGA 480
S L R L N R Y I S S T T N H F M T P V E
481 AACAACTCCAACCTGATTCTTCTTCTTCGTATCATTAGCTCTAATTCAATCATCATATCT 540
T T P T D S S S S S S L A L I Q S S Y L
541 ATCTCTAAACCAAGTTACCCCTTTCATAAGGTTTACTCAATTAACCGCTAATCAAGCGAT 600
S L N Q V T P F I R F T Q L T A N Q A I
601 TTTAGAAGCGATTAACGGTAATCATCAAGCAATCCACATCGTTGATTTGACATTAATCA 660
L E A I N G N H Q A I H I V D F D I N H

FIG.5A



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CGGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCCTGCTCCCACTC 720
G V Q W P P L M Q A L A D R Y P A P T L

721 TCGAATCACCGGTACTGGAAATGACCTTGATACCCTTCGTAGAACAGGTGATCGTTTAGC 780
R I T G T G N D L D T L R R T G D R L A

781 TAAATTTGCTCACTCATTAGGGTTGAGATTTCAATTCCATCCTCTTTATATAGCCAATAA 840
K F A H S L G L R F Q F H P L Y I A N N

841 TAACCACGATCACGATGAAGATCCTTCTATTATTTCTCCATTGTACTACTCCCTGATGA 900
N H D H D E D P S I I S S I V L L P D E

901 AACCTAGCTATCAACTGTGTTTTCTACCTCCACCGCCTTTTAAAAGACCGCGAAAAGTT 960
T L A I N C V F Y L H R L L K D R E K L

961 AAGGATTTTTTTGCATAGGGTTAAGTCAATGAACCCTAAAATTGTTACAATCGCGGAGAA 1020
R I F L H R V K S M N P K I V T I A E K

1021 GGAAGCAAATCATAACCATCCTCTTTTTTTTACAAAGATTCATCGAGGCGTTGGATTATTA 1080
E A N H N H P L F L Q R F I E A L D Y Y

1081 TACAGCTGTGTTTGATTCACTGGAAGCTACATTGCCACCGGGTAGTCGAGAGAGGATGAC 1140
T A V F D S L E A T L P P G S R E R M T

1141 AGTTGAACAAGTGTGGTTTGGGAGAGAGATTGTTGATATCGTTGCGATGGAAGGAGATAA 1200
V E Q V W F G R E I V D I V A M E G D K

1201 AAGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATT 1260
R K E R H E R F R S W E V M L R S C G F

FIG.5B



1261 TAGTAATGTTGCTTTAAGCCCTTTTGCATTATCACAAGCTAAGCTTCTTTTGAGACTTCA 1320
S N V A L S P F A L S Q A K L L L R L H

1321 TTATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATTCTTTCTTCTTAGGTTGGCA 1380
Y P S E G Y Q L G V S S N S F F L G W Q

1381 AAATCAACCCCTTTTCTCCATCTCGTGTTGGCGTTGAGAAAACTATCAAATAGCCAACT 1440
N Q P L F S I S S W R

1441 TCAGAGGGTAATTAAGACTACTGATAGTTTAGGAGGGATCTGAAGAAAACGCGTGGAGTG 1550

1501 AAAACCCTAAATAACCAGATTTTCTAATGAAGTTGTAGTAGTAGAAATTTGCATGGTGAA 1560

1561 GAACAATATTGAAGAGGTATTGAAATTTTCATGTTTTTTTTGTTTTACTTATTGATATGAA 1620

1621 TGTTTTAAAATTTTAAACATAGAGGACTAGGTTGATGATATATAGTATTTAAGTTAACTA 1680

1681 GTCTTTGTATAACGCAAGATCTTGATCAACTTATTTTTATTTTAAATTA 1729

FIG.5C

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1 ATGTTAGGATCCTTTGGTTCTTCATCATCTCAATCTCACCTCATCATGATGAAGAATCT 60
1 M L G S F G S S S S Q S H P H H D E E S 20
61 TCTGATCATCATCAACGGCGTAGATTCACCGCTACTACTACAACTATCACCACCACCACC 120
21 S D H H Q R R R F T A T T T T I T T T T 40
121 ACAACGACCTCACCAGCTATTCAAATCCGCCAGCTACTCATTAGCTGTGCGGAGTTGATT 180
41 T T T S P A I Q I R Q L L I S C A E L I 60
181 TCGCGGTCCGATTTCTCGGCCGCGAAAAGACTCCTTACCATATTATCAACTAACTCTTCT 240
61 S R S D F S A A K R L L T I L S T N S S 80
241 CCTTTTGGTGATTCAACTGAACGGTTAGTCCATCAGTTTACTCGCGCACTTTCCTTCGT 300
81 P F G D S T E R L V H Q F T R A L S L R 100
301 CTCAACCGCTATATATCGTCAACCACCAATCATTTTCATGACACCTGTTGAAACAACTCCA 360
101 L N R Y I S S T T N H F M T P V E T T P 120
361 ACTGATTCTTCATCTTCGTTGCCATCGTCATCATTAGCTCTAATTCAATCATCATATCAT 420
121 T D S S S S L P S S S L A L I Q S S Y H 140
421 TCTCTAAATCAAGTTACCCCTTTTATAAGGTTTACTCAATTAACCGCTAATCAAGCGATT 480
141 S L N Q V T P F I R F T Q L T A N Q A I 160
481 TTAGAAGCGATTAACGGTAATCATCAAGCAATCCACATCGTTGATTTGACATTAATCAC 540
161 L E A I N G N H Q A I H I V D F D I N H 180
541 GGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCCTGCTCCTACTCTT 600
181 G V Q W P P L M Q A L A D R Y P A P T L 200
601 CGAATCACCGGTACTGGAAATGACCTTGATACCCTTCGTAGAACAGGTGATCGTTTAGCT 660
201 R I T G T G N D L D T L R R T G D R L A 220

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FIG.6A



661 AAATTTGCTCACTCATTAGGGTTGAGATTTCAATTCATCCTCTTTATATCGCCAATAAT 720
221 K F A H S L G L R F Q F H P L Y I A N N 240
721 AACCGCGATCACGGTGAAGATCCTTCTATTATTTCTCCATTGTACTTCTCCCTGATGAA 780
241 N R D H G E D P S I I S S I V L L P D E 260
781 ACCCTAGCTATCAACTGTGTTTTCTATCTCCACCGCCTTTTAAAAGACCGCGAAAAATTA 840
261 T L A I N C V F Y L H R L L K D R E K L 280
841 AGGATTTTTTTGTCATAGGGTTAAGTCAATGAACCCTAAAATTGTTACAATCGCGGAGAAG 900
281 R I F L H R V K S M N P K I V T I A E K 300
901 GAAGCAAATCATAACCATCCTCTTTTTTTACAAAGATTTATCGAGGCGTTGGATTATTAT 960
301 E A N H N H P L F L Q R F I R A L D Y Y 320
961 ACAGCTGTGTTTGATTTCATTGGAAGCTACATTGCCACCGGGTAGTCGTGAGAGGATGACA 1020
321 T A V F D S L E A T L P P G S R E R M T 340
1021 GTTGAACAAGTGTGGTTTGGGAGAGAAATTGTTGATATCGTGGCGATGGAAGGAGATAAA 1080
341 V E Q V W F G R E I V D I V A M E G D K 360
1081 AGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATTT 1140
361 R K E R H E R F R S W E V M L R S C G F 380
1141 AGTAATGTTGCTTTAAGCCCTTTTGCATTATCACAAAGCTAAGCTTCTTTTGAGACTACAT 1200
381 S N V A L S P F A L S Q A K L L L R L H 400
1201 TATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATTCTTTCTTCTTAGGTTGGCAA 1260
401 Y P S E G Y Q L G V S S N S F F L G W Q 420
1261 AATCAACCTCTTTTCTCCATCTCGTCTTGGCGTTGA 1296
421 N Q P L F S I S S W R * 432

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FIG.6B



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1 GAGAGGTCATCAAACCCTAGCAGTCCACCTCCATCTCTCCGCATAACCGGATGCGGTGCA
E R S S N P S S P P P S L R I T G C G R
61 GATGTAACCGGATTAAACCGAACTGGAGACCGGTTAACCCGGTTCGCTGACTCTTTAGGT 120
D V T G L N R T G D R L T R F A D S L G
121 CTCCAATTCCAGTTTCACACGCTAGTGATCGTAGAAGAAGATCTCGCCGGACTTTTGCTA 180
L Q F Q F H T L V I V E E D L A G L L L
181 CAGATCCGATTGTTAGCTCTCTCAGCCGTACAAGGAGAGACCATTGCCGTCAATTGTGTT 240
Q I R L L A L S A V Q G E T I A V N C V
241 CACTTCCTCCACAAAATATTTAACGACGATGGAGATATGATCGGTCACTTCTTGTCAGCG 300
H F L H K I F N D D G D M I G H F L S A
301 ATCAAGAGCTTAAACTCTAGAATCGTTACAATGGCAGAGAGAGAAGCTAATCATGGAGAT 360
I K S L N S R I V T M A E R E A N H G D
361 CACTCGTTCTTGAATAGATTCTCTGAGGCAGTGGATCATTACATGGCGATCTTTGATTGCG 420
H S F L N R F S E A V D H Y M A I F D S
421 TTGGAAGCGACGTTGCCGCCAAATAGCCGAGAGAGACTAACCCTAGAGCAACGGTGGTTC 480
L E A T L P P N S R E R L T L E Q R W F
481 GGTAAGGAGATTTTGGATGTTGTGGCGGCGGAAGAGACGGAGAGAAAGCAAAGACATCGG 540
G K E I L D V V A A E E T E R K Q R H R
541 AGGTTTGAGATTTGGGAAGAGATGATGAAGAGGTTTGGTTTCGTTAACGTTCTATTGGA 600
R F E I W E E M M K R F G F V N V P I G
601 AGCTTTGCTTTGTCTCAAGCTAAGCTTCTTCTTAGACTTCATTATCCTTCAGAAGGTTAT 660
S F A L S Q A K L L L R L H Y P S E G Y
661 AATCTTCAGTTCCTTAACAATTCTTTG 687
N L Q F L N N S L

FIG.7



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LsAt	1	MLGSFGSSSSQSHPHHDEESSDHHQRRRTATATTTTTTTT	TTTSPAIIQRQLLISCAELI
LsLe	1	MLGSFGSSSSQSHPHHDEESSDHHQRRRTATATTTTTTTT	TTTSPAIIQRQLLISCAELI
LsSt	1	MLGSFGSSSSQSHPHHDEESSDHHQRRRTATATTTTTTTT	TTTSPAIIQRQLLISCAELI
LsAt	1	SSQDFSAKRLLTILSTNSSPFGDSTERLVHQFTRALSRLNRYISSTTNHFMTPVETTP	
LsLe	61	SSQDFSAKRLLTILSTNSSPFGDSTERLVHQFTRALSRLNRYISSTTNHFMTPVETTP	
LsSt	61	SSQDFSAKRLLTILSTNSSPFGDSTERLVHQFTRALSRLNRYISSTTNHFMTPVETTP	
LsAt	1	TDSSSS...SSSLALIQSSVLSLNQVTPFIRFTQLTANQAILEAINGNHQAIHIVDFDINH	
LsLe	121	TDSSSS...SSSLALIQSSVLSLNQVTPFIRFTQLTANQAILEAINGNHQAIHIVDFDINH	
LsSt	121	TDSSSS...SSSLALIQSSVLSLNQVTPFIRFTQLTANQAILEAINGNHQAIHIVDFDINH	
LsAt	1	ERSSNPSSPPSLRITGCGRUVGLNRTGURLIRFADSLGLQFQFHILMIVEE	
LsLe	178	GVQWPPPLMQALADRYAPATLRIITGTGNDLDTLRTGURLAKFAHSLGLRQFHPLYIANN	
LsSt	181	GVQWPPPLMQALADRYAPATLRIITGTGNDLDTLRTGURLAKFAHSLGLRQFHPLYIANN	
LsAt	54	DLAGLLQIRLLALSAVQGETIIVNCVHFHKIFNDJGDMIGHFLSAIKSLNSRIVTMAE	
LsLe	238	NHDEEDPSIISSIVLLPDETLAINCVFYLHRLK.DREKLRIFLHRVKSMPKIVITIAE	
LsSt	241	NRDHGEDPSIISSIVLLPDETLAINCVFYLHRLK.DREKLRIFLHRVKSMPKIVITIAE	
LsAt	114	REANHGDHSFLNRFSEAVDHYMAIFDSLEATLPPNSRERUTLEQRWFGKEILDVVAEET	
LsLe	297	KEANHNIHPLFLQRFIEALDYITAVFDSLEATLPPGSRERMTVEQWFGREIVDIVAMEGD	
LsSt	300	KEANHNIHPLFLQRFIEALDYITAVFDSLEATLPPGSRERMTVEQWFGREIVDIVAMEGD	

FIG. 8A



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LsAt	174	ERKQRRRFEIWEEMMKREGFVNVPIGSFALSOAKLLRLHYPSEGYNLOFLNNSL
LsLe	357	KRKERHERFRSWEVMLRSCGFSNVALSPFALSOAKLLRLHYPSEGYNLOFLNNSL
LsSt	360	KRKERHERFRSWEVMLRSCGFSNVALSPFALSOAKLLRLHYPSEGYNLOFLNNSL
LsAt	230	QNOPLFSISSMR*
LsLe	417	QNOPLFSISSMR*
LsSt	420	QNOPLFSISSMR*

FIG.8B